REMARKS

This is intended as a full and complete response to the Final Office Action dated January 23, 2008, having a shortened statutory period for response set to expire on April 23, 2008. Please reconsider the claims pending in the application for reasons discussed below.

Interview Summary

On March 21, 2007, a telephonic interview was conducted between the Examiner and Chance Hardie. Claim 1 was discussed with respect to being distinguished from the values for "Query Match" identified in Attachments 3 and 4 of the Office Action. While an agreement was not reached regarding patentability, the Examiner agreed to consider evidence as submitted herewith regarding the phrase "at least 96% identical," as recited in claim 1.

Claim Rejections - 35 U.S.C. § 102

Claims 1, 4 and 6 stand rejected under 35 U.S.C. § 102(b) as being anticipated by *Inouye et al.* Further, claims 1-2, 4-7, 11, 14, 18 and 21 stand rejected under 35 U.S.C. § 102(e) as being anticipated by *Stubbs et al.* In response, Applicants respectfully traverse the rejection.

Claim 1 recites that a nucleic acid molecule includes "a nucleic acid sequence which encodes a genetically engineered mutant" with "fluorescent properties and an amino acid sequence at least 96% identical to the *Aequorea coerulescens* non-fluorescent protein of SEQ ID NO: 2." As evidenced in the accompanying Declaration of Sergey Lukyanov, the "Query Match" values identified in Attachments 3 and 4 of the Office Action lack correspondence with the claimed phrase "at least 96% identical" and thus cannot provide the basis for anticipation of claim 1. Paragraphs [00105] and [00106] describe "sequence identity" as relating to percent "identical" and being "determined using MegAlign, DNAstar clustal algorithm as described in D. G. Higgins and P. M. Sharp, "Fast and Sensitive multiple Sequence Alignments on a Microcomputer," *CABIOS*, 5 pp. 151-3 (1989) (using parameters ktuple 1, gap penalty

3, window 5 and diagonals saved 5)." This MegAlign clustal algorithm is calculated by comparing two optimally aligned sequences, determining the number of positions at which the identical amino acid occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions, and multiplying the result by 100. (*See*, statement 6 of the Declaration.) The foregoing calculation defines the term "sequence identity" to one of ordinary skill in the art. (*See*, statement 7 of the Declaration.) Further, one of ordinary skill in the art would understand that the claim language "at least 96% identical" is determined by (number of amino acid matches) / (total number of amino acids) * 100, which is not the same as used to calculate the term "Query Match" upon which the Examiner bases the rejection. (*See*, statements 8 and 9 of the Declaration.) Rather than the values for the "Query Match," sequences shown in Attachments 3 and 4 of the final Office Action are respectively only 92.9% and 91.2% "identical" to SEQ ID NO: 2 referenced in claim 1.

As further evidence of the foregoing discussion being apparent to one of ordinary skill in the art, Applicants reference U.S. Patent 7,339,092 (the '092 patent). The '092 patent states in the first full paragraph of column 18 that "mathematical algorithms can be utilized for comparison of sequences to determine *sequence identity* (emphasis added)." Implementations of the algorithms include, according to the '092 patent, a "CLUSTAL program... well described by... Higgins et al. (1989) CABIOS 5:151-153" that is thus the same as referenced in the current specification. The '092 patent further states that "sequence identity" makes reference to the residues in the two sequences that are the same when aligned for maximum correspondence whereas "sequence *similarity* (emphasis added)" relates to corrections for conservative substitutions. (Column 19, lines 32-52). Therefore, a percentage of "sequence identity" (*i.e.*, as discussed at paragraphs [00105] and [00106] of the current specification and not percentage of sequence similarity) as stated at column 19, line 65, through column 20, line 4, of the '092 patent is "calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison, and multiplying the result by 100 to yield the percentage of sequence identity."

Therefore, the sequences taught in *Inouye et al.* or *Stubbs et al.* and identified by the Examiner are not "at least 96% identical to the *Aequorea coerulescens* non-fluorescent protein of SEQ ID NO: 2," as recited in claim 1. *Inouye et al.* or *Stubbs et al.* fail to teach, show or suggest each and every element of claim 1 and cannot anticipate claim 1 or any claims dependent thereon. Accordingly, Applicants request withdrawal of the rejections and allowance of claims 1-2, 4-7, 11, 14, 18 and 21.

Allowable Subject Matter

Claims 3, 24, 25, 39, 31 and 32 would be allowable if written in independent form. In response, Applicants submit that these claims are allowable based at least on the traversal presented herein regarding independent claim 1 from which the claims depend. Accordingly, Applicants request withdrawal of the objection and allowance of claims 3, 24, 25, 39, 31 and 32.

Claim 34 is allowed. Applicants acknowledge allowance of claim 34.

Withdrawn Claims

In view of the foregoing, Applicants submit that claim 1 is allowable. All withdrawn claims depend from claim 1. Accordingly, Applicants request withdrawal of the restriction requirement and allowance of the claims.

Specification

To correct a typographical error, Applicants have amended sequences identified as numbers 3-6 in the sequence listing to read GTT coding valine (V) in position 11 instead of GCT coding alanine (A). These amendments are supported by paragraphs [00165] and [00166] which state that "Mutant Z1 contained one amino acid substitution, E222G" and "Mutant Z2 contained two amino acid substitutions... N19D... and E222G." Accordingly, this corrective submission including the "Sequence Listing" on paper and in computer readable form (CRF) contains no new matter. Enclosed for filing in the above-referenced application is a paper copy of a "Sequence Listing" and a floppy disk containing a CRF of the "Sequence Listing." Applicants request amendment of the

specification to include the paper copy of the "Sequence Listing." The sequence listing information recorded in CRF is identical to the written on paper "Sequence Listing."

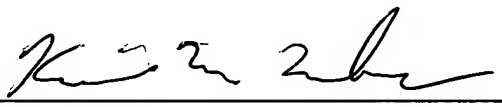
Drawings

To correct the same typographical error discussed above regarding the specification, Applicants have amended figures 3 and 5. The sequences illustrated in these figures now show GTT coding valine (V) in position 11 instead of GCT coding alanine (A). Again, these amendments contain no new matter and are supported by paragraphs [00165] and [00166].

Conclusion

Having addressed all issues set out in the office action, Applicant respectfully submits that the claims are in condition for allowance and respectfully request that the claims be allowed.

Respectfully submitted,



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